

Alignments

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>emb|V00866.1|HBVADW Hepatitis B virus complete DNA sequence (subtype adw)
Length=3200

Score = 5906 bits (3198), Expect = 0.0
Identities = 3198/3198 (100%), Gaps = 0/3198 (0%)
Strand=Plus/Plus

Query 3 TTCCACTGCCTTGCACCAAGCTCTGCAGGATCCCAGAGTCAGGGGTCTGTATCTTCTGCG 62
Sbjct 1 TTCCACTGCCTTGCACCAAGCTCTGCAGGATCCCAGAGTCAGGGGTCTGTATCTTCTGCG 60

Query 63 TGGTGGCTCCAGTTCAGGAACAGTAAACCTGCTCCGAATATTGCCTCTCACATCTCGTC 122
Sbjct 61 TGGTGGCTCCAGTTCAGGAACAGTAAACCTGCTCCGAATATTGCCTCTCACATCTCGTC 120

Query 123 AATCTCCGCGAGGACTGGGGACCTGTGACGATCATGGAGAATCATCATCAGGATTCTCT 182
Sbjct 121 AATCTCCGCGAGGACTGGGGACCTGTGACGATCATGGAGAATCATCATCAGGATTCTCT 180

Query 183 AGGACCCCTGCTCGTGTACAGCGGGGTTTTCTTGTGTGACAAGAATCCTCACAAATACC 242
Sbjct 181 AGGACCCCTGCTCGTGTACAGCGGGGTTTTCTTGTGTGACAAGAATCCTCACAAATACC 240

Query 243 GCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTCTAGGGGGATCACCCGTGTGCT 302
Sbjct 241 GCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTCTAGGGGGATCACCCGTGTGCT 300

Query 303 TGGCCAAAATTCGAGTCCCCAACCTCCAATCACTACCAACCTCTGCTCTCCAATTG 362
Sbjct 301 TGGCCAAAATTCGAGTCCCCAACCTCCAATCACTACCAACCTCTGCTCTCCAATTG 360

Query 363 TCCTGGTTATCGCTGGATGTGCTCGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCT 422
Sbjct 361 TCCTGGTTATCGCTGGATGTGCTCGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCT 420

Query 423 ATGCCTCATCTTCTTATTGGTTCTTCTGGATTATCAAGTATGTGTGCCCGTTTGTCCCTCT 482
Sbjct 421 ATGCCTCATCTTCTTATTGGTTCTTCTGGATTATCAAGTATGTGTGCCCGTTTGTCCCTCT 480

Query 483 AATTCCAGGATCAACAACACAGTACGGGACCATGCAAAACCTGCAGACTCCTGCTCA 542
Sbjct 481 AATTCCAGGATCAACAACACAGTACGGGACCATGCAAAACCTGCAGACTCCTGCTCA 540

Query 543 AGGCAACTCTAAGTTTCCCTCATGTTGCTGTACAAAACCTACGGATGGAAATGCACCTG 602
Sbjct 541 AGGCAACTCTAAGTTTCCCTCATGTTGCTGTACAAAACCTACGGATGGAAATGCACCTG 600

Query 603 TATTTCCCATCCCATCGTCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCTCAGTCCG 662
Sbjct 601 TATTTCCCATCCCATCGTCTGGGCTTTCGCAAAATACCTATGGGAGTGGGCTCAGTCCG 660

Query 663 TTTCTCTTGGCTCAGTTTACTAGTGCCATTGTTCAGTGGTTCGTAGGGCTTTCCCCCAC 722
Sbjct 661 TTTCTCTTGGCTCAGTTTACTAGTGCCATTGTTCAGTGGTTCGTAGGGCTTTCCCCCAC 720

Query 723 TGTTTGGCTTTCAGCTATATGGAATGATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGT 782
Sbjct 721 TGTTTGGCTTTCAGCTATATGGAATGATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGT 780

Query 783 GAGTCCCTTTATACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACATTTAAACCCCT 842
Sbjct 781 GAGTCCCTTTATACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACATTTAAACCCCT 840

Query 843 AACAAAACAAAAGATGGGGTTATTCCTAAACTTCATGGGCTACATAATTGGAAGTTGG 902
Sbjct 841 AACAAAACAAAAGATGGGGTTATTCCTAAACTTCATGGGCTACATAATTGGAAGTTGG 900

Query 903 GGAACCTTGGCCACAGGATCATATTGTACAAAAGATCAAAACACTGTTTATAGAAAACCTCCT 962
Sbjct 901 GGAACCTTGGCCACAGGATCATATTGTACAAAAGATCAAAACACTGTTTATAGAAAACCTCCT 960

Query 963 GTTAACAGGCCTATTGATTGGAAGTATGTCAAAGAATTGTGGGCTTTTGGGCTTTGCT 1022
Sbjct 961 GTTAACAGGCCTATTGATTGGAAGTATGTCAAAGAATTGTGGGCTTTTGGGCTTTGCT 1020

Query 1023 GCTCCATTTACAAATGTGGATATCTGCCTTAATGCCCTTTGTATGCAATGTATACAAGCT 1082
Sbjct 1021 GCTCCATTTACAAATGTGGATATCTGCCTTAATGCCCTTTGTATGCAATGTATACAAGCT 1080

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Query	1083	AAACAGGCTTTTCACTTTTCGCGCAACTTACAAGGCCTTTTCTAAGTAACAGTACATGAAC	1142
Sbjct	1081	AAACAGGCTTTTCACTTTTCGCGCAACTTACAAGGCCTTTTCTAAGTAACAGTACATGAAC	1140
Query	1143	CTTTACCCCGTTTGCTCGGCAACGGCTTGGTCTGTGCCAAGTGTGTTGCTGACGCAACCCCC	1202
Sbjct	1141	CTTTACCCCGTTTGCTCGGCAACGGCTTGGTCTGTGCCAAGTGTGTTGCTGACGCAACCCCC	1200
Query	1203	ACTGGCTGGGGCTTAGCCATAGGCCATCAGCGCATGCGTGGAACTTTTGTGGCTCCTCTG	1262
Sbjct	1201	ACTGGCTGGGGCTTAGCCATAGGCCATCAGCGCATGCGTGGAACTTTTGTGGCTCCTCTG	1260
Query	1263	CCGATCCATACATGCGGAACCTCTAGCCGCTTGTGTTTGTCTCGCAGCCGGTCTGGAGCAAAAG	1322
Sbjct	1261	CCGATCCATACATGCGGAACCTCTAGCCGCTTGTGTTTGTCTCGCAGCCGGTCTGGAGCAAAAG	1320
Query	1323	CTCATCGGAAGTGAACAATTCGTGCTCCTCTCGCGGAAATATACATCATTTCCATGGGCTG	1382
Sbjct	1321	CTCATCGGAAGTGAACAATTCGTGCTCCTCTCGCGGAAATATACATCATTTCCATGGGCTG	1380
Query	1383	CTAGGCTGTACTGCGCAACTGGATCCTTCGCGGGACGTCTTTGTTTACGTCCTCGGCGG	1442
Sbjct	1381	CTAGGCTGTACTGCGCAACTGGATCCTTCGCGGGACGTCTTTGTTTACGTCCTCGGCGG	1440
Query	1443	CTGAATCCCGCGGACGACCCCTCTCGGGGCGCTTGGGACTCTCTCGTCCCTTCTCCGT	1502
Sbjct	1441	CTGAATCCCGCGGACGACCCCTCTCGGGGCGCTTGGGACTCTCTCGTCCCTTCTCCGT	1500
Query	1503	CTGCCGTTCCAGCCGACACGGGGCGCACCTCTCTTTACGCGGTCTCCCGTCTGTGCCT	1562
Sbjct	1501	CTGCCGTTCCAGCCGACACGGGGCGCACCTCTCTTTACGCGGTCTCCCGTCTGTGCCT	1560
Query	1563	TCTCATCTGCCGGTCCGTGTGCACTTCGCTTACCTCTGCACGTTGCATGGCGACCACCG	1622
Sbjct	1561	TCTCATCTGCCGGTCCGTGTGCACTTCGCTTACCTCTGCACGTTGCATGGCGACCACCG	1620
Query	1623	TGAACGCCCATCAGATCCTGCCAAGGCTTTACATAAGAGGACTCTTGAGACTCCAGCAA	1682
Sbjct	1621	TGAACGCCCATCAGATCCTGCCAAGGCTTTACATAAGAGGACTCTTGAGACTCCAGCAA	1680
Query	1683	TGTCAACGACCGACCTTGAGGCCACTTCAAAGACTGTGTGTTAAAGGACTGGGAGGAGT	1742
Sbjct	1681	TGTCAACGACCGACCTTGAGGCCACTTCAAAGACTGTGTGTTAAAGGACTGGGAGGAGT	1740
Query	1743	TGGGGGAGGAGATTAGGTTAATGATCTTTGTATTAGGAGGCTGTAGGCATAAATTTGGTCT	1802
Sbjct	1741	TGGGGGAGGAGATTAGGTTAATGATCTTTGTATTAGGAGGCTGTAGGCATAAATTTGGTCT	1800
Query	1803	GCGCACCAGCACCATGCAACTTTTTACCTCTGCCTAATCACTCTTGTACATGTCAC	1862
Sbjct	1801	GCGCACCAGCACCATGCAACTTTTTACCTCTGCCTAATCACTCTTGTACATGTCAC	1860
Query	1863	TGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCATGGACATTGACCCTTATAA	1922
Sbjct	1861	TGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCATGGACATTGACCCTTATAA	1920
Query	1923	AGAATTTGGAGTACTGTGGAGTTACTCTCGTTTTTGGCTTCTGACTTCTTCCCTCCGT	1982
Sbjct	1921	AGAATTTGGAGTACTGTGGAGTTACTCTCGTTTTTGGCTTCTGACTTCTTCCCTCCGT	1980
Query	1983	ACGAGATCTCCTAGACACCGCTCAGCTCTGTATCGAGAAGCCTTAGAGTCTCCTGAGCA	2042
Sbjct	1981	ACGAGATCTCCTAGACACCGCTCAGCTCTGTATCGAGAAGCCTTAGAGTCTCCTGAGCA	2040
Query	2043	TTGCTCACCTCACCATACTGCACCTCAGGCAAGCCATTCTCTGCTGGGGGGAATTGATGAC	2102
Sbjct	2041	TTGCTCACCTCACCATACTGCACCTCAGGCAAGCCATTCTCTGCTGGGGGGAATTGATGAC	2100
Query	2103	TCTAGTACTCTGGTGGGTAATAATTTGCAAGATCCAGATCCAGAGATCTAGTAGTCAA	2162
Sbjct	2101	TCTAGTACTCTGGTGGGTAATAATTTGCAAGATCCAGATCCAGAGATCTAGTAGTCAA	2160
Query	2163	TTATGTTAATACTAACAATGGGTTTAAAGATCAGGCAACTATTGTGGTTTCATATATCTTG	2222
Sbjct	2161	TTATGTTAATACTAACAATGGGTTTAAAGATCAGGCAACTATTGTGGTTTCATATATCTTG	2220
Query	2223	CCTTACTTTTGGGAAGAGAGCTGTACTTGAATATTTGGTCTCTTTCGGAGTGTGGATTTCG	2282
Sbjct	2221	CCTTACTTTTGGGAAGAGAGCTGTACTTGAATATTTGGTCTCTTTCGGAGTGTGGATTTCG	2280
Query	2283	CACCTCTCAGCCTATAGACCACCAATGCCCTATCTTATCAACACTTCGGGAAACTAC	2342

Sbjct	2281	CACCTCCTCCAGCCTATAGACCACCAAAATGCCCTTATCTTATCAACACTTCCGGAAACTAC	2340
Query	2343	TGTTGTTAGACGACGGGACCGAGGCAAGTCCCTTAGAAGAAGAACTCCCTCGCCTCGCAG	2402
Sbjct	2341	TGTTGTTAGACGACGGGACCGAGGCAAGTCCCTTAGAAGAAGAACTCCCTCGCCTCGCAG	2400
Query	2403	ACGAGATCTCAATCGCCGCGTCGCAGAAGATCTCAATCTCGGGAAATCTCAATGTTAGTA	2462
Sbjct	2401	ACGAGATCTCAATCGCCGCGTCGCAGAAGATCTCAATCTCGGGAAATCTCAATGTTAGTA	2460
Query	2463	TTCTTTGGACTCATAAGGTCGGAAACTTTACGGGGCTTTATTTCCTCTACAGTACCTATCT	2522
Sbjct	2461	TTCTTTGGACTCATAAGGTCGGAAACTTTACGGGGCTTTATTTCCTCTACAGTACCTATCT	2520
Query	2523	TTAATCCTGAATGGCAAACCTCCTTCCTTTCTTAAGATTCAATTACAAGAGGACATTATTA	2582
Sbjct	2521	TTAATCCTGAATGGCAAACCTCCTTCCTTTCTTAAGATTCAATTACAAGAGGACATTATTA	2580
Query	2583	ATAGGTGTCAACAATTTGTGGGCCCCCTCACTGTAAATGAAAAGAGAAGATTGAAATTAA	2642
Sbjct	2581	ATAGGTGTCAACAATTTGTGGGCCCCCTCACTGTAAATGAAAAGAGAAGATTGAAATTAA	2640
Query	2643	TTATGCCTGCTAGATTCTATCCTACCCACACTAAATATTTGCCCTTAGACAAAGGAATTA	2702
Sbjct	2641	TTATGCCTGCTAGATTCTATCCTACCCACACTAAATATTTGCCCTTAGACAAAGGAATTA	2700
Query	2703	AACCTTATTATCCAGATCAGGTAGTTAATCATTACTTCCAAACAGACATTATTTACATA	2762
Sbjct	2701	AACCTTATTATCCAGATCAGGTAGTTAATCATTACTTCCAAACAGACATTATTTACATA	2760
Query	2763	CTCTTTGGAAGGCTGGTATTCTATATAAGAGGGAACCCACACGTAGCGCATCATTTTGGC	2822
Sbjct	2761	CTCTTTGGAAGGCTGGTATTCTATATAAGAGGGAACCCACACGTAGCGCATCATTTTGGC	2820
Query	2823	GGTCACCATATTTCTTGGGAACAAGAGCTACAGCATTCGCAAGGCATGGGGACGAACTTT	2882
Sbjct	2821	GGTCACCATATTTCTTGGGAACAAGAGCTACAGCATTCGCAAGGCATGGGGACGAACTTT	2880
Query	2883	TCTGTTCCCAACCCCTCTGGGATTCCCTCCCGATCATCAGTTGGACCCCTGCATTTCGGAGCC	2942
Sbjct	2881	TCTGTTCCCAACCCCTCTGGGATTCCCTCCCGATCATCAGTTGGACCCCTGCATTTCGGAGCC	2940
Query	2943	AACTCAACAAATCCAGATTGGGACTTCAACCCCATCAAGGACCACTGGCCAGCAGCCAAC	3002
Sbjct	2941	AACTCAACAAATCCAGATTGGGACTTCAACCCCATCAAGGACCACTGGCCAGCAGCCAAC	3000
Query	3003	CAGGTAGGAGTGGGAGCATTTCGGGCCAGGGCTCACCCCTCCACACGGCGGTATTTGGGG	3062
Sbjct	3001	CAGGTAGGAGTGGGAGCATTTCGGGCCAGGGCTCACCCCTCCACACGGCGGTATTTGGGG	3060
Query	3063	TGGAGCCCTCAGGCTCAGGGCATAATTGACCACAGTGTCAACAATTCCTCCTCCTGCCITC	3122
Sbjct	3061	TGGAGCCCTCAGGCTCAGGGCATAATTGACCACAGTGTCAACAATTCCTCCTCCTGCCITC	3120
Query	3123	ACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCTCCACCTCTAAGAGACAGTCAT	3182
Sbjct	3121	ACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCTCCACCTCTAAGAGACAGTCAT	3180
Query	3183	CCTCAGGCCATGCAGTGG	3200
Sbjct	3181	CCTCAGGCCATGCAGTGG	3198